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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/049,404

DATE: 07/11/2002  
TIME: 14:01:57

Input Set : A:\EP.txt  
Output Set: N:\CRF3\07112002\J049404.raw

3 <110> APPLICANT: Arndt, Michaela  
 4 Little, Melvyn  
 5 Kypriyanov, Sergey  
 6 Krauss, Jurgen  
 7 Pfreundschnuh, Michael  
 9 <120> TITLE OF INVENTION: Fv Antibody Construct Comprising Binding Sites For a CD16  
 Receptor and a  
 10 CD30 Surface Protein  
 12 <130> FILE REFERENCE: 4121-135  
 14 <140> CURRENT APPLICATION NUMBER: US 10/049,404  
 15 <141> CURRENT FILING DATE: 2002-02-05  
 17 <150> PRIOR APPLICATION NUMBER: PCT/DE00/02589  
 18 <151> PRIOR FILING DATE: 2000-08-02  
 20 <150> PRIOR APPLICATION NUMBER: DE 199 37 264  
 21 <151> PRIOR FILING DATE: 1999-08-06  
 23 <160> NUMBER OF SEQ ID NOS: 11  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 4570  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Artificial Sequence  
 32 <220> FEATURE:  
 33 <223> OTHER INFORMATION: Synthetic Construct  
 35 <400> SEQUENCE: 1  
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 40 atttcacaca gaattcatta aagaggagaa attaaccatg aaataccat tgcctacggc 180  
 42 agccgctggc ttgctgctgc tgccagctca gcccgcattgg cgccagggtc gctgcagcag 240  
 44 tctggagctg agctggtaag gcctggact tcagtgaaga tatcctgcaa ggcttctggc 300  
 46 tacacccatca ctaactactg gctaggttgg gtaaaacaga ggcctggaca tggactcgag 360  
 48 tggattggag atatctaccc tgaggtgttatactactaact acaatgagaa attcaaggc 420  
 50 aaggccacag tgactgcaga cacatcctcc agaactgcct acgtgcaggc caggagcctg 480  
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 54 tggggcgcac ggactacggt caccgtctcc tcagccaaaa caacacccaa gcttggcggt 600  
 56 gatatcgagc tcactcagtc tccaaaattt atgtccacat cagtaggaga cagggtcaac 660  
 58 gtcacctaca aggccagtca gaatgtgggt actaatgttag cctggttca aaaaaacca 720  
 60 gggcaatctc ctaaaggcttct gatattactcg gcatcttacc gatacagtgg agtccctgtat 780  
 62 cgcttcacag gcagtggatc tgaacagat ttcaactctca ccatcagcaa tgtgcagtct 840  
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 66 ggcaccaagc tggaaatcaa acgggctgtat gctgcggccg ctggatccga aaaaaagctg 960  
 68 atctcagaag aagacctaata ctcacatcac catcaccatc actaaagatc tattaaagag 1020  
 70 gagaattaa ccatgaaata cctattgcct acggcagccg ctggcttgc gctgctggca 1080  
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78 aatccctagca	gtggatattc	tgactacaat	cagaacttca	agggcaagac	cacattgact	1320
80 qcagacaagt	cctccaaacac	agcctacatg	caactgaaca	gcctgacatc	tgaggactct	1380
82 gcggtctatt	actgtcaag	aagagcggac	tatggtaact	acgaatatac	ctgggttgct	1440
84 tactggggcc	aagggaccac	ggtcaccgtc	tcctcagcca	aaacaacacc	caagcttggc	1500
86 ggtgatatcc	aggctttgt	gactcagaa	tctgcactca	ccacatcacc	tggtgaaaca	1560
88 gtcacactca	tttgcgtc	aaatactgg	actgttacaa	ctagtaacta	tgccaaactgg	1620
90 gtccaaagaaa	aaccagatca	tttattact	ggtctaatacg	gtcataccaa	caaccgagct	1680
92 ccaggtgttc	ctgcccattt	ctcaggctcc	ctgattggag	acaaggctgc	cctcaccatc	1740
94 acaggggcac	agactgagga	tgaggcaata	tatttctgtg	ctctatggta	taacaaccat	1800
96 tgggtgttcg	gtggagaaac	caaactgact	gtccttaggc	agcccaagtc	tgccggccgct	1860
98 ggatccgaac	aaaagctgat	ctcagaagaa	gacctaaact	cacatcacca	tcaccatcac	1920
100 taatcttagag	gcctgtgcta	atgatcagct	agcttgaggc	atcaataaaa	cgaaggctc	1980
102 agtcgaaaga	ctgggccttt	cgttttatct	gttgggttc	ggtaacgtc	gacccggcgt	2040
104 aatagcgaga	ggcccgcacc	gatcccccctt	cccaacagtt	gcgcagcctg	aatggcgaat	2100
106 gggacgcgccc	ctgttagcggc	gcattaagcg	cgccgggtgt	ggtggttacg	cgcacgtga	2160
108 ccgtctacact	tgccagcgcc	ctagcgcggc	ctccttcgc	tttcttcct	tcctttctcg	2220
110 ccacgttcgc	cggcttcccc	cgtcaagctc	taaatcgggg	gctccctta	gggttccgat	2280
112 ttagtgcattt	acggcacctc	gaccccaaaaa	aacttgatta	gggtgatgg	tcacgtatgt	2340
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118 tataaggat	tttgcgatt	tcggcctatt	ggttaaaaaa	tgagctgatt	taacaaaaat	2520
120 ttaacgcgaa	ttttaacaaa	atattaacgc	ttacaattt	ggtggcactt	ttcggggaaa	2580
122 tgcgcgcca	acccttattt	gtttatttt	ctaaatata	tcaaataatgt	atccgctcat	2640
124 gagacaataa	ccctgataaa	tgcttcaata	atattgaaaa	aggaagagta	tgagtattca	2700
126 acatttccgt	gtcgccctta	ttcccttttt	tgccgcattt	tgcccttcgt	tttttgctca	2760
128 cccagaaacg	ctgggtgaaag	taaaagatgc	tgaagatcag	ttgggtgcac	gagtgggtta	2820
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134 cgggcaagag	caactcggtc	gccgcataca	ctattctcg	aatgacttgg	ttgagtactc	3000
136 accagtccaca	gaaaagcatac	ttacggatgg	catgacagta	agagaattat	gcagtgcgtc	3060
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140 ggagctaacc	gttttttgc	acaacatggg	ggatcatgta	actcgcttgc	atcggtggga	3180
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144 ggcaacaacg	ttgcgc当地	tattaactgg	cgaaactactt	actctagctt	cccgcaaca	3300
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148 ggctggctgg	tttattgtcg	ataaatctgg	agccggtag	cgtgggtc	gcccgtatcat	3420
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164 cagcagagcg	cagataccaa	atactgtct	tctagtgt	ccgtagttag	gccaccactt	3900
166 caagaactct	gtagcaccgc	ctacatactt	cgctctgtca	atcctgtac	cagtggtgc	3960
168 tgccagtgcc	gataagtcgt	gtcttacccg	gttggactca	agacgatagt	taccggataa	4020
170 ggcgcagcgg	tcgggtcgaa	cggggggttc	gtgcacacag	cccagcttgg	agcgaacgac	4080
172 ctacaccgaa	ctgagaacct	acagcgtgag	ctatgagaaa	gcccacgct	tcccgaaagg	4140

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174 agaaaaggcgg acaggttatcc ggtaagcggc agggtcggaa caggagagcg cacgagggag 4200  
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 180 gcccgccttt tacgggttgc ggcctttgc tggccttttgc ctcacatgtt ctttcctgc 4380  
 182 ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga taccgctgc 4440  
 184 cgcagccgaa cgaccgagcg cagcgagtcg gtgagcggagg aagcggaaaga gcccgcata 4500  
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 202 1 5 10 15  
 205 Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr  
 206 20 25 30  
 209 Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu  
 210 35 40 45  
 213 Trp Ile Gly Asp Ile Tyr Pro Gly Gly Tyr Thr Asn Tyr Asn Glu  
 214 50 55 60  
 217 Lys Phe Lys Gly Lys Ala Thr Val Thr Ala Asp Thr Ser Ser Arg Thr  
 218 65 70 75 80  
 221 Ala Tyr Val Gln Val Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
 222 85 90 95  
 225 Phe Cys Ala Arg Ser Ala Ser Trp Tyr Phe Asp Val Trp Gly Ala Arg  
 226 100 105 110  
 229 Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly  
 230 115 120 125  
 233 Asp Ile Glu Leu Thr Gln Ser Pro Lys Phe Met Ser Thr Ser Val Gly  
 234 130 135 140  
 237 Asp Arg Val Asn Val Thr Tyr Lys Ala Ser Gln Asn Val Gly Thr Asn  
 238 145 150 155 160  
 241 Val Ala Trp Phe Gln Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile  
 242 165 170 175  
 245 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly  
 246 180 185 190  
 249 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser  
 250 195 200 205  
 253 Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr His Thr Tyr Pro Leu  
 254 210 215 220  
 257 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala  
 258 225 230 235 240  
 261 Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser  
 262 245 250 255  
 265 His His His His His  
 266 260

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270 <211> LENGTH: 273  
271 <212> TYPE: PRT  
272 <213> ORGANISM: Artificial Sequence  
274 <220> FEATURE:  
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277 <400> SEQUENCE: 3  
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284 20 25 30  
287 Thr Tyr Thr Ile His Trp Val Arg Gln Arg Pro Gly His Asp Leu Glu  
288 35 40 45  
291 Trp Ile Gly Tyr Ile Asn Pro Ser Ser Gly Tyr Ser Asp Tyr Asn Gln  
292 50 55 60  
295 Asn Phe Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr  
296 65 70 75 80  
299 Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
300 85 90 95  
303 Tyr Cys Ala Arg Arg Ala Asp Tyr Gly Asn Tyr Glu Tyr Thr Trp Phe  
304 100 105 110  
307 Ala Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr  
308 115 120 125  
311 Thr Pro Lys Leu Gly Gly Asp Ile Gln Ala Val Val Thr Gln Glu Ser  
312 130 135 140  
315 Ala Leu Thr Thr Ser Pro Gly Glu Thr Val Thr Leu Thr Cys Arg Ser  
316 145 150 155 160  
319 Asn Thr Gly Thr Val Thr Ser Asn Tyr Ala Asn Trp Val Gln Glu  
320 165 170 175  
323 Lys Pro Asp His Leu Phe Thr Gly Leu Ile Gly His Thr Asn Asn Arg  
324 180 185 190  
327 Ala Pro Gly Val Pro Ala Arg Phe Ser Gly Ser Leu Ile Gly Asp Lys  
328 195 200 205  
331 Ala Ala Leu Thr Ile Thr Gly Ala Gln Thr Glu Asp Glu Ala Ile Tyr  
332 210 215 220  
335 Phe Cys Ala Leu Trp Tyr Asn Asn His Trp Val Phe Gly Gly Thr  
336 225 230 235 240  
339 Lys Leu Thr Val Leu Gly Gln Pro Lys Ser Ala Ala Ala Gly Ser Glu  
340 245 250 255  
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344 260 265 270  
347 His  
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353 <212> TYPE: DNA  
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357 <223> OTHER INFORMATION: Synthetic Construct  
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RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\EP.txt  
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VERIFICATION SUMMARY

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